



(19)

Europäisches Patentamt

European Patent Office

Office européen des brevets



41/4/00

(11)

EP 0 984 061 A1

(12)

EUROPEAN PATENT APPLICATION

published in accordance with Art. 158(3) EPC

(43) Date of publication:

08.03.2000 Bulletin 2000/10

(51) Int. Cl.⁷: **C12N 9/24**, C12N 15/56,
C12N 5/10

// (C12N9/24, C12R1:91)

(21) Application number: 98919547.4

(22) Date of filing: 11.05.1998

(86) International application number:
PCT/JP98/02072

(87) International publication number:
WO 98/53052 (26.11.1998 Gazette 1998/47)

(84) Designated Contracting States:
DE ES GB IT

(30) Priority: 22.05.1997 JP 13217497

(71) Applicant: MIYAGI KEN
Sendai-shi, Miyagi 980 (JP)

(72) Inventors:
• MIYAGI, Taeko
Miyagi Cancer Center
Natori-shi Miyagi 981-1293 (JP)

• WADA, Tadashi
Miyagi Cancer Center
Natori-shi Miyagi 981-1293 (JP)
• YOSHIKAWA, Yuko
Miyagi Cancer Center
Natori-shi Miyagi 981-1293 (JP)

(74) Representative:
Bannerman, David Gardner et al
Withers & Rogers,
Goldings House,
2 Hays Lane
London SE1 2HW (GB)

(54) SIALIDASES LOCALIZED ON PLASMA MEMBRANES AND DNA ENCODING THE SAME

(57) Sialidases localized on plasma membranes as shown in the following (A) or (B): (A) a protein having an amino acid sequence represented by SEQ ID NO: 2 or 4; or (B) a protein derived from the protein (A) by substitution, deletion, insertion or transition of one or several amino acids in the amino acid sequence represented by SEQ ID NO: 2 or 4 and having the activity of removing a sialate residue from the non-reducing end of ganglioside.

EP 0 984 061 A1

Descripti n

Technical Field

- 5 [0001] The present invention provides a novel sialidase and DNA coding for it. More precisely, the present invention provides sialidase that localizes in plasma membrane, and specifically hydrolyzes gangliosides, and DNA coding for it. [0002] The sialidase of the present invention and the DNA coding for it are expected to be utilized as a reagent used for saccharide chain studies and a medicament used for gene diagnosis and gene therapy.

10 Background Art

[0003] Sialidase is a glycohydrolytic enzyme present in living bodies, which eliminates a sialic acid residue from a non-reducing terminal of saccharide chains of glycoproteins or glycolipids. It has been known that, when sialic acid is removed from saccharide chain molecules, not only the degradation of these molecules begins, but also molecular conformation and many of important cell functions such as recognition mechanism by receptors, cell adhesion, and immu-
 15 nomechanism may be changed. It has also become clear that sialidase exhibits rapid activity change in connection with proliferation and canceration of cells, and it is involved in the metastatic ability of cancer cells. However, there is little knowledge about how sialic acid is eliminated *in vivo*. This is because the studies of mammalian sialidases on the molecular level are behindhand, and hence there are many unknown points concerning their structures and expression mechanism.

[0004] Because mammalian sialidase exhibits only low activity, and is extremely unstable, isolation and purification of the enzyme have been difficult. Sialidase has been often considered for a long time to be one of the mere lysosomal enzymes involved in the dissimulation and degradation. Under such a situation, we isolated and purified the enzyme by using mainly rat tissues as the source of the enzyme, and found that there were four types of sialidases which differ from
 25 sialidases of bacteria, viruses, protozoa and the like in their natures (Miyagi, T. and Tsuiki, S., *Eur. J. Biochem.* 141, 75-81, 1984; Miyagi, T. *et al.*, *J. Biochem.* 107, 787-793, 1990; Miyagi, T. and Tsuiki, S., *J. Biol. Chem.* 260, 6710-6716, 1985). These enzymes each localize in lysosomal matrix, lysosome membrane, plasma membrane (cell surface membrane), and cytoplasm within a cell, respectively, and they are different from each other not only in enzymological characteristics such as substrate specificity, but also in immunological properties. Among those sialidases, the sialidase
 30 localized in cytoplasm can be obtained as a homogenous purified product from rat skeletal muscles. Its cDNA cloning has been succeeded for the first time in the world as for animal sialidases, and its primary structure has been determined (Miyagi T. *et al.*, *J. Biol. Chem.*, 268, 26435-26440, 1993). Its genomic structure analysis has also been done, and as for its function, it has been elucidated that the enzyme participates in the differentiation and the growth of skeletal muscle cells by using the cDNA as a probe. These studies can be considered a part of pioneer researches in sialidase studies in the world.

[0005] By the previous studies, it has become clear that there is possibility that the sialidase localized in plasma membrane exhibits activity elevation upon proliferation and canceration of cells, and it is also deeply concerned with the differentiation of nerve cells and the signal transduction of cells. To date, however, it has not been understood at all about the structure of this enzyme, the mechanism causing the activity change and the like. In order to answer these ques-
 40 tions, what many researchers in this field have long been desired is cloning of its cDNA. For example, if the mechanism of cancerous change due to this enzyme could be elucidated, it would be possible to utilize the results in diagnosis and therapy of cancers. Further, because gangliosides exist in surface membranes of many cells and participate in important cell functions such as cell adhesion and informational communication, and they are also main cerebral components, the sialidase utilizing them as a specific substrate is estimated to be involved in certain important cranial nerve functions.

Summary of the Invention

[0006] The present invention has been accomplished in view of the aforementioned present condition. An object of
 50 the present invention is to provide the sialidase localized in plasma membrane and DNA that codes for it.

[0007] The inventors of the present invention earnestly conducted studies in order to achieve the aforementioned object, and as a result, succeeded in isolating the sialidase localized in plasma membrane and cloning of cDNA coding for it. Furthermore, they found that the aforementioned sialidase was unique in that it substantially specifically hydro-
 55 lyzed gangliosides (glycolipids containing sialic acid), which are substrates that similarly localize mainly in plasma membrane, and it was completely different from other mammalian sialidases and microbial sialidases in enzymatic substrate specificity. Thus, they accomplished the present invention.

[0008] That is, the present invention provides a protein defined in the following (A) or (B):

- (A) a protein which has the amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4, or
 (B) a protein which has the amino acid sequence including substitution, deletion, insertion, or transition of one or several amino acid residues in SEQ ID NO: 2 or SEQ ID NO: 4, and exhibits activity to eliminate a sialic acid residue from a non-reducing terminal of ganglioside.

5

[0009] The present invention also provides DNA coding for the protein defined in the above (A) or (B). Specifically, such DNA may be DNA which has the nucleotide sequence of SEQ ID NO: 1 or SEQ ID NO: 3.

[0010] A sialidase which has the aforementioned characteristics will be referred to as the "sialidase of the present invention" hereinafter, and DNA coding for it will be referred to as the "DNA of the present invention" hereinafter.

10

[0011] Hereafter, the present invention will be explained in detail.

(1) Sialidase of the present invention

15

[0012] The sialidase of the present invention is a protein which has the amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4. Moreover, the sialidase of the present invention includes a protein which has the amino acid sequence including substitution, deletion, insertion, or transition of one or several amino acid residues in SEQ ID NO: 2 or SEQ ID NO: 4, so long as it exhibits activity for eliminating a sialic acid residue from a non-reducing terminal of ganglioside.

[0013] Among the aforementioned sialidases, the sialidase that has the amino acid sequence of SEQ ID NO: 2 has the following physicochemical properties.

20

(1) Activity

[0014] It eliminates sialic acid residues from a non-reducing terminal of ganglioside.

25

(2) substrate specificity

30

[0015] It acts on gangliosides, but not act on glycoproteins and oligosaccharides. Specifically, it acts on GD3-ganglioside, GD1a-ganglioside, GM3-ganglioside, and synthetic gangliosides (GSC-17(α 2-3) and GSC-61(α 2-6)), but it does not substantially act on GM2-ganglioside, GM1-ganglioside, orosomucoid, fetuin, glycophorin, ovine submaxillary gland mucin, and bovine submaxillary gland mucin. It weakly acts on α 2-3 sialyllactose, and 4-MUNeuAc (4-methylumbelliferyl N-acetylneuraminic acid).

(3) Optimum pH

35

[0016] 4.7 to 5.0

(4) Molecular weight

[0017] About 65,000 as determined by sucrose density gradient centrifugation.

40

[0018] About 52,000 as determined by SDS-polyacrylamide gel electrophoresis under reducing condition

(5) Inhibition and activation

45

[0019] A surface active agent is required for the activity. For example, it is highly active in the presence of 0.1 to 0.2% of Triton X-100.

[0020] It is strongly inhibited by heavy metal ions such as Cu^{2+} , and 4-hydroxy mercury benzoate.

[0021] It is stabilized by dithiothreitol, Neu5Ac2en (2-deoxy-2,3-dehydro-N-acetylneuraminic acid), and glycerol. However, it is weakly inhibited by Neu5Ac2en.

50

[0022] Among the sialidases of the present invention, the sialidase which has the aforementioned characteristics is an enzyme derived from bovine, whereas the sialidase which has the amino acid sequence of SEQ ID NO: 4 in one derived from human. These exhibit 82% homology in their amino acid sequences, and they have a transmembrane domain, glycosylation site, and Asp-box, which is a consensus sequence of sialidase, at the same locations. Therefore, the enzyme derived from human is considered to have the same physicochemical properties as the enzyme derived from bovine.

55

[0023] The sialidase of the present invention can be obtained from a bovine brain, for example, as follows. All of the following procedures are preferably carried out at a low temperature.

[0024] A bovine brain is homogenized in a buffer, and centrifuged at 1000 x g for 10 minute, and the supernatant is further centrifuged at 30,000 x g for 1 hour. After the centrifugation, the precipitate fraction is suspended in a buffer,

added 5% deoxycholic acid, sufficiently homogenized, and centrifuged at 100,000 x g for one hour to obtain a soluble fraction as a supernatant. The buffer preferably contains an inhibitor for proteases, dithiothreitol, surface active agent and the like.

5 [0025] The above soluble fraction is applied to a DEAE-cellulose column and, after the column is washed, eluted with a buffer containing 0.2 M NaCl for fractionation. A fraction exhibiting the sialidase activity is dialyzed against a buffer, then applied on Octyl-Sepharose, and separated by elution with a linear gradient of 0.1-0.4% Triton X-100.

[0026] Then, an active fraction is applied to Heparin-Sepharose (Pharmacia), washed with a buffer containing 0.25 M NaCl, and eluted with a 0.2-1 M NaCl linear gradient to concentrate the active fraction. The above concentrated enzyme solution is loaded on Sephacryl S-200 (Pharmacia), and separated by elution with a buffer containing 0.02 mM
10 NeuAc2en (2-deoxy-2,3-dehydro-N-acetylneuraminic acid).

[0027] The obtained active fraction is diluted to have a Triton X-100 concentration of 0.02%, added to RCA-lectin agarose (Pharmacia), washed with a buffer containing 0.02% Triton X-100, and eluted with a buffer containing 0.2 M lactose. This active fraction is loaded on a MonoQ (Pharmacia) column, and eluted with a 0-0.5 M NaCl linear gradient.

[0028] The active fraction is loaded on an activated thiol Sepharose (Pharmacia) column, washed with a 0.15 M NaCl buffer containing 10% glycerol, and then with 0.5 M NaCl buffer containing 10% glycerol, and eluted with 0.05 M NaCl
15 buffer containing 0.05 M dithiothreitol. The active fraction is concentrated in a MonoQ column.

[0029] The above concentrate is loaded on an affinity column utilizing a synthetic ganglioside GM3 [GSC-211, NeuAc-Gal-Glc-O(CH₂)₈NH₂] as a ligand (Hasegawa A. et al. J. Carbohydr. Chem., 9, 201-214, 1990), and separated by elution with a 0-0.5 M NaCl gradient. The affinity column can be obtained by allowing GSC-211 to couple with ECH-Sepha-
20 rose (Pharmacia) in the presence of N-ethyl-N'-(3'-dimethyl-aminopropyl)carbodiimide hydrochloride.

[0030] The sialidase enzyme is purified as described above as a protein having a molecular weight of 52 kD as determined by SDS-polyacrylamide gel electrophoresis.

[0031] Further, since DNA coding for the sialidase of the present invention has been obtained, the sialidase of the present invention can also be obtained by expressing the DNA in a suitable host-vector system. As for the host-vector
25 system, a cultured cell can be used as a host, and a vector suitable for this host can be used. Materials and methods therefore may be those usually used for the production of heterogenous proteins utilizing genetic recombination techniques. When DNA coding for the sialidase of the present invention is ligated to a vector, a vector containing sequences required for regulation of gene expression such as promoter and terminator that can be expressed in the host as required may be used.

30 (2) DNA of the present invention

[0032] Because the amino acid sequence of the protein encoded by the DNA of the present invention has been elucidated, the DNA of the present invention can be cloned based on the amino acid sequence. In the examples mentioned
35 below, a partial amino acid sequence of the sialidase of the present invention is determined, oligonucleotide primers are synthesized based on the partial amino acid sequence, and the DNA of the present invention is obtained from a bovine brain cDNA library by PCR (polymerase chain reaction) using the oligonucleotides primers.

[0033] Although the sequence of the DNA of the present invention is not particularly limited so long as it codes for the amino acid sequence of SEQ ID NO: 2 or 4, the nucleotide sequences of SEQ ID NO: 1 and 3 can be specifically mentioned. Further, existence of sialidases having the amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4 including
40 substitution, deletion, insertion, or transition of one or several amino acid residues, and genes coding for them is expected due to difference of animal species, individuals or varieties. Such DNA coding for the substantially same protein as the sialidase of the present invention also falls within the scope of the DNA of the present invention. Such DNA can also be obtained from a cell harboring it by hybridizing it with the nucleotide sequence of SEQ ID NO: 1 or 3 or a part thereof under a stringent condition, and isolating DNA coding for a protein which has sialidase activity. DNA coding
45 for a sialidase having such a mutation as mentioned above may also be obtained by, for example, site-specific mutagenesis or mutagenic treatment.

[0034] The term "one or several" amino acid residues means 1-80, preferably 1-30, more preferably 1-5 amino acid residues.

50 (3) Progressive applications of the sialidase of the present invention and DNA coding for it

[0035]

55 (1) Because the sialidase of the present invention exhibits substrate specificity unique in that it substantially specifically hydrolyze gangliosides, a recombinant having the enzyme or DNA coding for the enzyme has much possibility for use as a reagent for saccharide chain studies.

(2) As one of the means for normalizing abnormality of this enzyme observed in cancer cells, for example, anti-

sense therapy, which is a kind of gene therapy, will be expected in future. The gene structure clarified by the present invention is the important information for it. Moreover, if the expression mechanism of this enzyme becomes clear by genome structure analysis utilizing the cDNA as a probe, it will also become possible to normalize the abnormality of the expression of this enzyme in cancer and the like.

(3) Because of two reasons, i.e., the characteristic that the enzyme specifically decomposes gangliosides that are main components of brain, and its involvement in differentiation of nerve cells, the abnormalities of this enzyme may be found in certain brain diseases. In such a case, the information about the gene may be much utilized for development of gene therapy and medicaments.

10 Brief description of the Drawings

[0036]

Fig. 1 represents the amino acid sequences of peptides obtained by endoproteinase digestion and lysyl endopeptidase digestion. The amino acids represented with minor characters in the figure are amino acids of low determinancy. A Lys residue presumed to have bound to the N-terminus amino acid is represented with (K).

Fig. 2 represents alignment of deduced amino acid sequences of a PCR product (BBmSD) obtained by using bovine brain cDNA as a template and a rat skeletal muscle cytoplasmic sialidase (RMcSD). Common amino acids are represented with dots ".", and analogous amino acids are represented with asterisks "*". The highly homologous regions used for the preparation of a probe are underlined.

Rest Mode for Carrying Out the Invention

[0037] Hereafter, the present invention will be explained more specifically with reference to the following examples.

(1) Purification of sialidase localized in plasma membrane

(1) Method for measuring sialidase activity

[0038] In this example, sialidase activity was measured as follows.

[0039] A reaction system (0.2 ml) contained 50-100 nmol of sialic acid-bound saccharide substrate, 0.2 mg of bovine serum albumin, 15 mmol of sodium acetate buffer (pH 4.6), 0.2 mg of Triton X-100, and an enzyme fraction, and a substrate consisting mainly of bovine brain mixed gangliosides (Sigma, Type II) was used.

[0040] A reaction mixture having the aforementioned composition was incubated at 37°C for 15-60 minutes, and the reaction was stopped by quick freezing. The released sialic acid was quantitated by the thiobarbituric acid method of Warren (Warren L., *J. Biol. Chem.* 234, 1971-1975, 1959) at 549 nm and 532 nm. In Steps 1, 2, and 7 explained below, the quantitation was performed by the same method after the reaction product was passed through an AGX-2 ion exchange mini column. The amount of the sialic acid (nmol) released per hour was defined as 1 unit. When a synthetic substrate, 4-methylumbelliferyl N-acetylneuraminic acid (4MU-NeuAc) was used as the sialic acid-bound saccharide substrate, Triton X-100 was excluded from the reaction system, and released 4-methylumbelliferone was quantitated by a fluorospectrophotometer.

[0041] In this example, the amount of enzyme protein was measured by the Bradford method (a kit of Biorad Co. was used), or the BCA method (Pierce Chemical Co.). Further details of the measuring methods are found in the previous report (Miyagi and Tsuiki, *J. Biol. Chem.* 260, 6710-6716, 1985).

(2) Solubilization and purification of bovine membrane-bound sialidase

[0042] The whole procedure described below was carried out at 4°C. Bovine brains obtained from a slaughterhouse were frozen at -80°C until they were used.

[0043] 200 g of bovine brain was added 9 volumes of 0.32 M sucrose, 1 mM DTT (dithiothreitol), 1 mM EDTA, and 0.1 mM PMSF (phenylmethylsulfonyl fluoride), homogenized by a glass Teflon homogenizer, and centrifuged at 1000 x g for 10 minute. The resulting supernatant was further centrifuged at 30,000 x g for 1 hour. After the centrifugation, the resulting precipitate fraction (Step 1) was suspended in Buffer A (20 mM potassium phosphate, pH 6.8, 0.1% Triton X-100, 1 mM EDTA, 1 mM DTT) containing 180 ml of 0.1 mM PMSF, then added 5% deoxycholic acid, sufficiently homogenized, and centrifuged at 100,000 x g for one hour to obtain a supernatant as a soluble fraction (Step 2).

[0044] The soluble fraction was applied to a DEAE-cellulose column (4.5 x 20 cm) equilibrated with Buffer A, washed, and eluted with Buffer A containing 0.2 M NaCl to collect 15 ml-fractions (Step 3). The active fraction was dialyzed against Buffer A, then applied to an Octyl-Sepharose column (2.5 x 7 cm) equilibrated with the same buffer, and eluted

with a linear gradient (400 ml) of 0.1-0.4% Triton X-100 to collect 10-ml fractions (Step 4).

[0045] Then, the active fraction was applied to a Heparin-Sepharose column (1.5 x 1 cm), washed with Buffer A containing 0.25 M NaCl, and eluted with a 0.2-1 M NaCl linear gradient (200 ml) in Buffer A, and the active fraction was concentrated by ultrafiltration using a YM-10 membrane (Step 5).

5 [0046] Concentrated enzyme solution obtained from 3 times of the elution from the Heparin-Sepharose column was loaded on a Sephacryl S-200 column (Pharmacia, 1.5 x 2.5 cm.), and eluted with Buffer B (20 mM potassium phosphate, pH 6.8, 0.04% Triton X-100, 1 mM EDTA, 1 mM DTT, 0.02 mM NeuAc2en [2-deoxy-2,3-dehydro-N-acetyl-neuraminic acid]) at a flow rate of 10 ml/h to collect 2-ml fractions (Step 6).

10 [0047] The active fraction from Step 6, which was diluted so that it should have a Triton X-100 concentration of 0.02%, was applied to an RCA-lectin agarose column (1.5 x 2.5 cm) equilibrated with Buffer B in which only the concentration of Triton X-100 was changed to 0.02%, washed with the same buffer, and eluted with Buffer B containing 0.2 M lactose (Step 7). This active fraction was applied to a MonoQ (HR 5/5) column (Pharmacia), eluted with a 0-0.5 M NaCl linear gradient in Buffer B, and stored at -20°C (Step 8).

15 [0048] The fraction obtained from 3 times of the elution in Step 8 (corresponding to 1.8 kg of the starting material) was loaded on an activated thiol-Sepharose column (Pharmacia, 1.5 x 2 cm), and eluted with Buffer B containing 0.15 M NaCl and 10% glycerol, and then with Buffer B containing 0.5 M NaCl and 10% glycerol, and eluted with Buffer B containing 0.5 M NaCl and DTT at a concentration raised to 50 mM. The active fraction was concentrated with a MonoQ column as in Step 8 (Step 9).

20 [0049] Finally, affinity column chromatography utilizing a synthetic ganglioside GM3 [GSC-211, NeuAc-Gal-GlcO(CH₂)₈NH₂] (Hasegawa A. *et al.*, *J. Carbohydr. Chem.*, 9, 201-214, 1990) as a ligand was performed. An affinity column (0.7 x 3 cm) was prepared by allowing the GSC-211 to couple to ECH-Sepharose (Pharmacia) in the presence of N-ethyl-N'-(3'-dimethyl-aminopropyl)carbodiimide hydrochloride according to the instruction of the manufacturer. The enzyme fraction obtained from Step 8 was loaded on the column equilibrated with Buffer C (10 mM potassium phosphate, pH 6.8, 0.04% Triton X-100, 1 mM EDTA, 1 mM DTT, 20% glycerol), and eluted with a 0-0.5 M NaCl concentration gradient in Buffer C to collect 1.5 ml-fractions (Step 10).

25 [0050] The purification process using 3.5 kg of bovine brains as the start material was summarized in Table 1. By the procedure explained above, the sialidase activity was purified by more than 100,000 times from the bovine brain particulate fraction. The final sample was subjected to SDS-polyacrylamide gel electrophoresis according to the method of Laemmli (Laemmli, U.K. *Nature*, 227, 680-685, 1970) to determine its purity. As a result, while a weak band at 50k was observed other than the main 52k protein band, the staining density of the 52k protein was parallel with the activity elution pattern from the affinity column, and in addition, this band was concentrated from Step 9 to 10. Therefore, it was considered to be a sialidase enzyme protein.

Table 1

Step	Total amount of proteins (mg)	Total activity (Unit)	Specific activity (Unit/mg)	Purification degree (-fold)	Yield (%)
Particulate fraction	36622	1666327	45.5	1	100
40 Solubilized fraction	23057	1616337	70.1	1.5	97
DEAE-cellulose	13440	1051740	78.3	1.7	63
Octyl-cellulose	1581	486000	307	6.7	29
45 Heparin-Sepharose	112	245520	2188	48	15
Sephacryl S-200	4.51	44670	9926	218	2.6
RCA-lectin agarose	0.521	25771	49464	1087	1.5
50 Mono Q	0.220	19590	89045	1957	1.2
Activated-thiol Sepharose	0.0103	18660	1811650	39816	1.1
55 Ganglioside - Sepharose	0.0012	5773	4851260	106621	0.34

(3) Physicochemical properties of bovine membrane-bound sialidase

[0051] The physicochemical properties of the enzyme investigated by using the aforementioned purified enzyme are shown below.

(i) Substrate specificity

[0052] The results of investigations about the activity of the enzyme of the present invention for various substrates are shown in Table 2. The numerical values represent relative activity when the activity for the GD3-ganglioside is defined to be 100.

Table 2

Substrate	Hydrolysis activity (%)
Ganglioside	
GD3-ganglioside	100
GD1a-ganglioside	56
GM3-ganglioside	62
GM2-ganglioside	3
GM1-ganglioside	1
Synthetic ganglioside	
GSC-17 (α 2-3)	110
GSC-61 (α 2-6)	44
Orosomucoid	2
Fetuin	2
Glycophorin	3
Ovine submaxillary gland mucin	3
Bovine submaxillary gland mucin	0
α 2-3 sialyllactose	11
4-MUNeuAc	25

[0053] The hydrolysis of GSC-17 (α 2-3) occurred at a rate 2.5 times higher than that of the hydrolysis of GSC-61 (α 2-6), and hence the enzyme is considered to be more likely to act on α 2-3 linkage compared with α 2-6 linkage. Further, since it did not act on α 2-3 sialyllactose corresponding to the saccharide segment of the GM3 ganglioside, the ceramide segment is indispensable for a substrate.

(ii) Optimum pH

[0054] 4.7 to 5.0

(iii) Molecular weight

[0055] About 65,000 as determined by sucrose density gradient centrifugation.

[0056] About 52,000 as determined by SDS-polyacrylamide gel electrophoresis under reducing condition.

(iv) Inhibition, activation etc.

[0057] A detergent is required for the activity. For example, it is highly active in the presence of 0.1 to 0.2% of Triton X-100.

[0058] Residual activities in the presence of various inhibitors are shown in Table 3. The numerical values each rep-

resent 100 minus (residual activity (%) in the presence of inhibitor).

Table 3

Inhibitor	Inhibition (%)
CuCl ₂ (1 mM)	95
4-Hydroxy mercury benzoate (50 μM)	92
2-Deoxy-2,3-dehydro-N-acetylneuraminic acid (0.2 mM)	45

(3) Peptide sequencing

[0059] Because the above-obtained final product was obtained at a low yield, the enzyme fraction of Step 9 was prepared in a similar manner by using 6 kg of bovine brains as the starting material, and subjected to peptide analysis. The enzyme fraction was desalted by dialysis in the presence of 0.1% PVP-40 (sigma), concentrated with Centricon (Millipore), subjected to SDS-polyacrylamide gel electrophoresis as described above, and transferred to a PVDF membrane (Problott, Applied Biosystems). The location of the enzymatic protein was confirmed by Ponceau S staining, and the corresponding part of the membrane was excised, and digested with lysyl endopeptidase and then with endoproteinase Asp-N. The product was separated by high performance liquid chromatography.

[0060] The fractionated peptide was subjected to amino acid sequencing using a peptide sequencer (Shimazu PSQ-1). The above microsequencing was performed according to the method of Iwamatsu *et al.* (Iwamatsu A. and Yoshida-Kubomura N., *J. Biochem.* 120, 29-34, 1996). The obtained sequences are represented in Fig. 1 and SEQ ID NOS: 5-9. SEQ ID NOS: 5-7 are amino acid sequences of the fragments obtained by the endoproteinase digestion, and SEQ ID NOS: 8 and 9 are amino acid sequences of the fragments obtained by the lysyl endopeptidase digestion. In SEQ ID NO: 5, the 2-5th amino acids are indefinite, and it is highly possible that the 2nd amino acid should be Ala or Arg, the 3rd amino acid be Glu or Gly, the 4th amino acid be Ile or Tyr, and the 5th amino acid be Leu or Ser.

(2) cDNA cloning of bovine brain sialidase

[0061] Based on the amino acid sequence of the peptide of the purified enzyme, which had been determined as described above, 10 sense or antisense degenerate primers of SEQ ID NOS: 10 (DN1-1S), 11 (DN1-1A), 12 (DN1-2S), 13 (DN1-2A), 14 (DN2S), 15 (DN2A), 16 (DN3A), 17 (AP1A), 18 (AP3S), and 19 (AP3A) were prepared (see Fig. 1). DN1, DN2, DN-3, AP-1, and AP-3 are designations of the peptides shown in Fig. 1, S means "sense", and A means "antisense". DN-1 represents a nucleotide sequence determined by assuming that the indefinite amino acids of DN-1 (the 2-5th amino acids) should be Ala, Glu, Ile, and Leu, respectively, and DN-2 represents a nucleotide sequence determined by assuming that the indefinite amino acids of DN-1 should be Arg, Gly, Tyr, and Ser, respectively.

[0062] Bovine brain total RNA was prepared by the acid guanidium-phenol-chloroform method (Chomczynski P. and Sacchi N., *Anal. Biochem.* 162, 156-159, 1987), and poly(A)⁺RNA was purified by oligo(dT)-cellulose column chromatography. cDNA was prepared in accordance with the previous report (Miyagi T. *et al.*, *J. Biol. Chem.*, 268, 26435-26440, 1993) using the poly(A)⁺RNA (1 mg) and reverse transcriptase (derived from Molony murine leukemia virus, BRL), and amplification by PCR utilizing the cDNA as a template was attempted.

[0063] The PCR reaction mixture (50 μl) had a composition of 50 mM KCl, 10 mM Tris-HCl (pH 8.3), 1.5 mM MgCl₂, 0.01% of gelatin, 0.2 mM dNTPs (2 mM each of dATP, dGTP, dCTP and dTTP), 0.5 mg of cDNA, and 1.5 units of Taq polymerase (Ex Taq, Takara). The DNA amplification was performed by 40 cycles of reactions of at 94°C (0.5 minutes), 50°C (1 minute) and 72°C (2 minutes), followed by extension reaction at 72°C for 10 minutes. The obtained 12 DNA amplification fragments were each subcloned in the *Sma*I site of Bluescript vector (Stratagene), and subjected to DNA sequencing by the dideoxy method (Sanger F. *et al.*, *Proc. Natl. Acad. Sci. USA*, 74, 5463-5467, 1977).

[0064] As a result of examination for the validity of the amino acid sequences deduced from the nucleotide sequences of the segments corresponding to the primers within the amplified DNA fragments, presence or absence of a stop codon and the like, it was found that only a PCR product of 0.5 kb obtained with primers AP3S and DN2A fulfilled those requirements. In addition, two Asp-boxes (-Ser-Xaa-Asp-Xaa-Gly-Xaa-Thr-Trp- (SEQ ID NO: 20)), which is a consensus sequence of sialidase, were found in this fragment (amino acid numbers 131-138 and 205-212 in SEQ ID NO: 2), and the deduced amino acid sequence exhibited 38% homology with respect to the amino acid sequence of the cytoplasmic sialidase, which we had previously isolated. However, it did not exhibit significant homology with any other proteins.

[0065] Then, a bovine brain λgt10 library (Clontech) was screened by using the above 0.5 kb cDNA as a probe. The cDNA was isotope-labeled with [α-³²P]dCTP using Random Primer DNA Labeling Kit (Takara), and phages (2 × 10⁶)

were screened by plaque hybridization. The hybridization was carried out by using a nylon membrane (Hybond N⁺, Amersham) according to the instruction of the manufacturer. Among 15 positive clones, two of pBB121 (1.45 kb) and pBB321 (2.8 kb) were estimated to contain the full coding region.

5 [0066] The nucleotide sequence of the insert of pBB321 (2.8 kb) and the amino acid sequence deduced from it are shown as SEQ ID NOS: 1 and 2. It was found that four types of amino acid sequences obtained from the peptide of the purified product were contained in it, and as for DN-1, the 2nd amino acid of DN 1-1 was A R. Moreover, because it was found that the same sequence was contained in bovine keratin based on protein database search, although it was not found for the AP-1 sequence, it is highly possible that it originated from contamination of keratin in the enzyme fraction used for the peptide sequencing.

10 [0067] In addition to the above-mentioned two Asp-boxes, another Asp-box was further found on their 3' side (the amino acid numbers 256-263 in SEQ ID NO: 2). A hydrophobic sequence considered to be a transmembrane domain was found between the two Asp-boxes (the amino acid numbers 174-194 in SEQ ID NO: 2), and a glycosylation site was found on its 3' side (the amino acid number 349 in SEQ ID NO: 2). Because the enzyme has the characteristic that it is bound to RCA lectin as used in the purification procedure, it is considered that a saccharide chain actually attached
15 to this site. The molecular weight of the protein calculated from the 428 amino acids is 48,000, and if one saccharide chain is attached, the actual value will become around 50,000, and it is not contradictory to the value determined for the above purified product by SDS-polyacrylamide gel electrophoresis.

(3) Transient expression of sialidase cDNA in COS cell

20 [0068] The coding region of pBB121 (1.45 kb) was amplified by PCR using 5' sense primer (SEQ ID NO: 21) which was added an *Eco*RI site and 3' antisense primer (SEQ ID NO: 22), and the obtained DNA fragment was purified by agarose electrophoresis. This product was ligated to the *Eco*RI site of SR α promoter high expression vector pME18S (provided by Dr. Kazuo Maruyama, Medical Department, Tokyo Medical and Dental University) having SV40 replication
25 origin (pME18S-mSD), and introduced into COS-7 cells by electroporation to attempt its transient expression. Forty μ g of pME18S or pME18S-mSD was added to COS-7 cells (10^5) cultured in DMEM containing 10% FBS (fetal bovine serum) in the logarithmic growth phase, left at room temperature for 10 minutes, applied with electric pulses at 250 V and 950 μ FD, left at room temperature again for 10 minutes, and then returned to the culture.

[0069] The cells after the culture of 48 hours were collected. After the blood serum components were removed with
30 PBS, the cells were added 9 volumes of PBS, and disrupted by ultrasonication for 10 seconds. The disrupted cell suspension was centrifuged under cooling at 1,000 x g for 10 minutes, and the resulting supernatant was used as a homogenate. Sialidase activity in the homogenate of the transfectants was measured by using gangliosides as the substrate in the presence of Triton X-100 (0.1%).

[0070] The specific activity of control cells having only the vector and the cells that were introduced with pME18S-
35 mSD was 23.4 units/mg protein and 844.5 units/mg protein, respectively. Thus, the cells introduced with pME18S-mSD exhibited the activity 36 times higher than that of the control cells. However, increase of the activity for hydrolyzing 4MU-sialic acid was not observed at all. This result confirmed the results of the previous characterization of the purified product of the bovine brain enzyme, *i.e.*, the expressed sialidase substantially specifically acted on gangliosides, and hardly acted on synthetic substrates such as 4MU-sialic acid.

40 [0071] Further, it was investigated whether the expressed sialidase localized in plasma membrane or not by using Percoll (Pharmacia) concentration gradient centrifugation. In accordance with a previous report (Sagawa J. *et al.*, *J. Biochem.* 107, 452-456, 1990), the homogenate was overlaid on 40% Percoll containing 0.25 M sucrose, centrifuged at 48,000 x g for 40 minutes, and fractionated, and the sialidase activity was measured. Ganglioside sialidase activity was detected at the same location as the activity distribution of 5'-nucleotidase or alkali phosphatase, which are marker
45 enzymes of plasma membrane, and thus the localization of the expressed sialidase in plasma membrane was confirmed.

(4) cDNA cloning of human-derived ganglioside sialidase

50 [0072] When the primary structure of the bovine brain sialidase was compared with the previously isolated cytoplasmic sialidase (Miyagi T. *et al.*, *J. Biol. Chem.*, 268, 26435-26440, 1993), it was found that they contained a sequence well conserved in them (Fig. 2). Therefore, one set of primers was prepared based on this amino acid sequence (SEQ ID NOS: 23 and 24). In the amino acid sequences shown in Fig. 2, the partial sequence of cDNA for bovine brain sialidase (BBmSD) corresponds to the amino acid numbers 49-209 of SEQ ID NO: 2. The rat skeletal muscle cytoplasmic
55 sialidase (RMmSD) corresponds to the amino acid numbers 1-240 in the amino acid sequence of the sialidase.

[0073] Human brain cDNA and human kidney cDNA were prepared under the same condition as the case of the bovine enzyme, and PCR was performed by using them as the template. The amplified DNA fragment of 0.25 kb was subcloned, and the DNA sequence was determined. One Asp-box was found in this cDNA. A human brain λ gt10 cDNA

library and human kidney λ gt10 cDNA library (Clontech) were screened by using the above DNA as a probe. By screening 8×10^5 plaques for human brain and 1×10^6 plaques for human kidney, three positive clones (pHB82, pHB85, and pHB95) and one positive clone (pHK65) were obtained, respectively.

5 [0074] When these DNA sequences were investigated after subcloning, an overlapped portion of 1 kb was found in all of them. Nucleotide sequences obtained from pHB95 containing the substantially whole coding region and pHK65 containing 3' end non-coding region of 1 kb, and deduced amino acid sequences therefor are shown as SEQ ID NOS: 3 and 4. They exhibited high homology with the sequences for bovine brain enzyme, *i.e.*, 81% (87% for only the coding region) on the nucleotide level, and 82% on the amino acid level.

10 [0075] In SEQ ID NO: 4, the transmembrane domain corresponds to the amino acid numbers 174-194, the glycosylation site to the amino acid number 348, and the Asp-boxes to the amino acid numbers 131-138, 205-212, and 256-263.

[0076] When the expression status was investigated in various human tissues by Northern blotting using the 1.5 kb insert of pHB95 as the probe, high expression of mRNA of about 4 kb was observed in skeletal muscles, and mRNA of the same size was also detected in brain, liver and the like.

15 Industrial Availability

[0077] The present invention provides sialidase localized in plasma membrane and DNA coding for it. The sialidase of the present invention differs from sialidases known so far in that it mainly localizes in plasma membrane, and specifically hydrolyze gangliosides.

20

25

30

35

40

45

50

55

SEQUENCE LISTING

5 <110> Miyagiken

<120> SIALIDASE LOCALIZED IN PLASMA MEMBRANE AND
DNA CODING FOR THE SAME

10 <130> OP699

<140>

15 <141> 1999-11-

<150> JP 9-132174

20 <151> 1997-05-22

<160> 24

25 <170> PatentIn Ver. 2.0

<210> 1

<211> 3003

30 <212> DNA

<213> Bos primigenius taurus

<220>

35 <221> CDS

<222> (259)..(1542)

<400> 1

40 ggagcttcct ggacttcctt tctaacggc tgtttcggc ttccccaatc tgcagcccc 60

gccgccagcc tctcgatgc tctgtcgcc tgtttttca ctttcgtgg ttgtgtccg 120

45 cgtccgcagt ttctctctg cctctgttc cagggttga tcatttcca gggttcagt 180

gtcggagacg tgagtgttg acccagcgc cagatcagcc cgagagagat ggaggagccg 240

50 gggttcctg cagagtc atg gaa gaa gtg aca tca tgc tcc ttc agc agc 291

Met Glu Glu Val Thr Ser Cys Ser Phe Ser Ser

55

	1	5	10	
5	cct ctg ttc cag cag gag gac aag aga ggg gtc acc tac cgg atc cca	339		
	Pro Leu Phe Gln Gln Glu Asp Lys Arg Gly Val Thr Tyr Arg Ile Pro			
	15	20	25	
10	gcc ctg atc tac gtg ccc cct gcc cac acc ttc ctg gcc ttt gca gag	387		
	Ala Leu Ile Tyr Val Pro Pro Ala His Thr Phe Leu Ala Phe Ala Glu			
	30	35	40	
15	aag cgc tcc tcg agc aag gat gag gat gct ctc cac ctg gtg ctg agg	435		
	Lys Arg Ser Ser Ser Lys Asp Glu Asp Ala Leu His Leu Val Leu Arg			
	45	50	55	
20	cga gga tta agg act ggg caa tca gta cag tgg gaa ccc ctg aag tcc	483		
	Arg Gly Leu Arg Thr Gly Gln Ser Val Gln Trp Glu Pro Leu Lys Ser			
	60	65	70	75
25	ctg atg aaa gcc acg tta cct gga cac cgg acc atg aac ccc tgt cct	531		
	Leu Met Lys Ala Thr Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro			
	80	85	90	
30	gtg tgg gag cgg aag agt ggc tac gtg tac ctg ttc ttc atc tgt gtg	579		
	Val Trp Glu Arg Lys Ser Gly Tyr Val Tyr Leu Phe Phe Ile Cys Val			
	95	100	105	
35	caa ggc cat gtc acc gag cgt caa cag att atg tca ggc agg aac cct	627		
	Gln Gly His Val Thr Glu Arg Gln Gln Ile Met Ser Gly Arg Asn Pro			
	110	115	120	
40	gca cgc ctc tgc ttc ata tgc agc cag gat gct ggc tat tca tgg agt	675		
	Ala Arg Leu Cys Phe Ile Cys Ser Gln Asp Ala Gly Tyr Ser Trp Ser			
	125	130	135	
45	gat gtg agg gac ctg act gag gag gtc att ggc cca gag gtg aca cac	723		
	Asp Val Arg Asp Leu Thr Glu Glu Val Ile Gly Pro Glu Val Thr His			
	140	145	150	155
50	tgg gcc act ttt gct gtg ggg cca ggt cat ggc atc cag ctg cag tcg	771		
	Trp Ala Thr Phe Ala Val Gly Pro Gly His Gly Ile Gln Leu Gln Ser			
	160	165	170	
55				

5 ggg agg ctc atc atc cct gca tat gcc tac tac atc ccg ttc tgg ttc 819
 Gly Arg Leu Ile Ile Pro Ala Tyr Ala Tyr Tyr Ile Pro Phe Trp Phe
 175 180 185

10 ttt tgc ttt cgg ctg cca tat aga gct agg cct cat tcc ctg atg atc 867
 Phe Cys Phe Arg Leu Pro Tyr Arg Ala Arg Pro His Ser Leu Met Ile
 190 195 200

15 tat agc gat gac cta gga gcc aca tgg cac cat ggc agg ctt atc aag 915
 Tyr Ser Asp Asp Leu Gly Ala Thr Trp His His Gly Arg Leu Ile Lys
 205 210 215

20 ccc atg gtg aca gtg gaa tgt gaa gtg gca gag gtg atc ggg aag gcc 963
 Pro Met Val Thr Val Glu Cys Glu Val Ala Glu Val Ile Gly Lys Ala
 220 225 230 235

25 ggc cac cct gtg ctg tat tgc agt gcc cgg aca cca aac agg cac cgg 1011
 Gly His Pro Val Leu Tyr Cys Ser Ala Arg Thr Pro Asn Arg His Arg
 240 245 250

30 gca gag gcc ctc agc att gac cat ggt gaa tgc ttt cag aaa cca gtc 1059
 Ala Glu Ala Leu Ser Ile Asp His Gly Glu Cys Phe Gln Lys Pro Val
 255 260 265

35 ctg agc cat cag ctc tgt gag ccc cct cat ggc tgt caa ggc agt gtg 1107
 Leu Ser His Gln Leu Cys Glu Pro Pro His Gly Cys Gln Gly Ser Val
 270 275 280

40 gtg agt ttc tgt ccc ctg gag atc cca ggt gga tgc cag gat ctt gct 1155
 Val Ser Phe Cys Pro Leu Glu Ile Pro Gly Gly Cys Gln Asp Leu Ala
 285 290 295

45 ggc gaa gat gca cct gcc att cag cag agt cct ctg ctg tgc agc tca 1203
 Gly Glu Asp Ala Pro Ala Ile Gln Gln Ser Pro Leu Leu Cys Ser Ser
 300 305 310 315

50 gtg aga cca gag ccg gaa gct gga acc ctg tca gaa tca tgg ctc ttg 1251
 Val Arg Pro Glu Pro Glu Ala Gly Thr Leu Ser Glu Ser Trp Leu Leu
 320 325 330

55

5 tac tca cac cca acc aat aag aaa cgg agg gtc gat cta ggc atc tac 1299
 Tyr Ser His Pro Thr Asn Lys Lys Arg Arg Val Asp Leu Gly Ile Tyr
 335 340 345

10 ctc aac cag agc ccc ttg gag gct gcc tgc tgg tcc cgc ccc tgg atc 1347
 Leu Asn Gln Ser Pro Leu Glu Ala Ala Cys Trp Ser Arg Pro Trp Ile
 350 355 360

15 ttg cac tgc ggg ccc tgt ggg tac tct gat ttg gct gct ctg gag aat 1395
 Leu His Cys Gly Pro Cys Gly Tyr Ser Asp Leu Ala Ala Leu Glu Asn
 365 370 375

20 gag ggc ttg ttt ggg tgt ttg ttt gaa tgt ggg acc aag cag gag tgt 1443
 Glu Gly Leu Phe Gly Cys Leu Phe Glu Cys Gly Thr Lys Gln Glu Cys
 380 385 390 395

25 gag cag att gcc ttc cgc ctg ttt aca gac cga gag atc ctg agc cac 1491
 Glu Gln Ile Ala Phe Arg Leu Phe Thr Asp Arg Glu Ile Leu Ser His
 400 405 410

30 gtg caa ggg gac tgc tcc acc cct ggt atg aac tct gag cca agt aaa 1539
 Val Gln Gly Asp Cys Ser Thr Pro Gly Met Asn Ser Glu Pro Ser Lys
 415 420 425

35 aag taattcgctt aggaccaac ttgcataga aggctaccgt agaaggcagt 1592
 Lys

40 cacagccagg acagtggagg ccaggataac agaggttact gaagtctgca gagaacaaa 1652
 acacctaata ttctgtctcc tacctgtttt cacttctcat tctccagaga acaaaatgaa 1712
 catcttgcca tagctactgc attcaaaaga gcactgaacg gtgagctgag agactatgat 1772

45 gtcactcttg ctcttccact ggcttgcttt gggaccttg acatgtcacc tgtactctct 1832
 gggcctcagg tctccatctg taaaaggaga gggctcgatc tctgatttct cttcttccca 1892

50 tccctaggaa aggcagtgtg cctgcatgcc cctgatcag caagtccctg ctgtatgtag 1952
 gactcttate tcaaaggcag gctccgcttt tcaaagtact tgccactcat ccaagtataa 2012

55

ggttacaagc aggtgtcata gcacaaagga agatgtaggt ggcctgtttt gttttaata 2072
 5 acaaaagcac ttacatcctt ctgattatgc acgaagctct acagactcac tgttctagag 2132
 gaatcgggcc aagcagcaga attataggtc acttaccttc tccagcttta cagctctgct 2192
 10 ccacctttcc ttccctgtcc agaaagcatt acctctgaag gaaaaatga gatgtcnaat 2252
 gtcagtatc ttcaataatg gtacttaatg tttctgtgg catgactcct atgagagatg 2312
 15 aacttgaagt tcatttatta gtagattat tgatgagaaa tgaacatggg ttaggacttc 2372
 aaagcatcgg aaaaaacttt ctgctattgc tgctctcaag gagttcacag ttagggggc 2432
 20 tagaagaggg ataaaattga agaaaataaa ttagctggg gggatagttt atagatattg 2492
 ggctctaagt gggagtata gtactgtctg atggtattat ttaattgta tcttaattgt 2552
 25 gcttgagtc atctcccca gaactgtcc aagctgctgt ttgtttttct cagaatgttg 2612
 ttttactca gccttcttta atggagacag tcgtcaccat tcagaaggtc tctggactca 2672
 30 aaaacctctg aatcaagcat atttgttcag acctactgaa atttggacca tctctactat 2732
 tagtgaagt tagagatgct tctttatcta atagatttgg gataaacttt gacattgctg 2792
 35 gttctcagat gatagcagat ggttgcctt attttagatc atttctcca taagcctttt 2852
 actgtgacag atactcttat tgtgagagct acctttttt tccctatttt tggaggataa 2912
 40 tgccttaaac aggcagcagg taaatatatt tgggtgctgag taatgacctt ggagagtaag 2972
 tcgttgcgt ggaacacagc ctagaaagt g 3003

45 <210> 2
 <211> 428
 <212> PRT
 50 <213> Bos primigenius

 <400> 2

55

Met Glu Glu Val Thr Ser Cys Ser Phe Ser Ser Pro Leu Phe Gln Gln
 1 5 10 15
 5
 Glu Asp Lys Arg Gly Val Thr Tyr Arg Ile Pro Ala Leu Ile Tyr Val
 20 25 30
 10
 Pro Pro Ala His Thr Phe Leu Ala Phe Ala Glu Lys Arg Ser Ser Ser
 35 40 45
 15
 Lys Asp Glu Asp Ala Leu His Leu Val Leu Arg Arg Gly Leu Arg Thr
 50 55 60
 20
 Gly Gln Ser Val Gln Trp Glu Pro Leu Lys Ser Leu Met Lys Ala Thr
 65 70 75 80
 25
 Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro Val Trp Glu Arg Lys
 85 90 95
 30
 Ser Gly Tyr Val Tyr Leu Phe Phe Ile Cys Val Gln Gly His Val Thr
 100 105 110
 35
 Glu Arg Gln Gln Ile Met Ser Gly Arg Asn Pro Ala Arg Leu Cys Phe
 115 120 125
 40
 Ile Cys Ser Gln Asp Ala Gly Tyr Ser Trp Ser Asp Val Arg Asp Leu
 130 135 140
 45
 Thr Glu Glu Val Ile Gly Pro Glu Val Thr His Trp Ala Thr Phe Ala
 145 150 155 160
 50
 Val Gly Pro Gly His Gly Ile Gln Leu Gln Ser Gly Arg Leu Ile Ile
 165 170 175
 55
 Pro Ala Tyr Ala Tyr Tyr Ile Pro Phe Trp Phe Phe Cys Phe Arg Leu
 180 185 190
 60
 Pro Tyr Arg Ala Arg Pro His Ser Leu Met Ile Tyr Ser Asp Asp Leu
 195 200 205
 65
 Gly Ala Thr Trp His His Gly Arg Leu Ile Lys Pro Met Val Thr Val
 210 215 220

5 Glu Cys Glu Val Ala Glu Val Ile Gly Lys Ala Gly His Pro Val Leu
 225 230 235 240

 Tyr Cys Ser Ala Arg Thr Pro Asn Arg His Arg Ala Glu Ala Leu Ser
 245 250 255

 10 Ile Asp His Gly Glu Cys Phe Gln Lys Pro Val Leu Ser His Gln Leu
 260 265 270

 15 Cys Glu Pro Pro His Gly Cys Gln Gly Ser Val Val Ser Phe Cys Pro
 275 280 285

 20 Leu Glu Ile Pro Gly Gly Cys Gln Asp Leu Ala Gly Glu Asp Ala Pro
 290 295 300

 Ala Ile Gln Gln Ser Pro Leu Leu Cys Ser Ser Val Arg Pro Glu Pro
 305 310 315 320

 25 Glu Ala Gly Thr Leu Ser Glu Ser Trp Leu Leu Tyr Ser His Pro Thr
 325 330 335

 30 Asn Lys Lys Arg Arg Val Asp Leu Gly Ile Tyr Leu Asn Gln Ser Pro
 340 345 350

 35 Leu Glu Ala Ala Cys Trp Ser Arg Pro Trp Ile Leu His Cys Gly Pro
 355 360 365

 40 Cys Gly Tyr Ser Asp Leu Ala Ala Leu Glu Asn Glu Gly Leu Phe Gly
 370 375 380

 Cys Leu Phe Glu Cys Gly Thr Lys Gln Glu Cys Glu Gln Ile Ala Phe
 385 390 395 400

 45 Arg Leu Phe Thr Asp Arg Glu Ile Leu Ser His Val Gln Gly Asp Cys
 405 410 415

 50 Ser Thr Pro Gly Met Asn Ser Glu Pro Ser Lys Lys
 420 425

 55

<210> 3
 <211> 1892
 5 <212> DNA
 <213> Homo sapiens

 <220>
 10 <221> CDS
 <222> (11)..(1294)

 <400> 3
 15 tgcagaggtc atg gaa gaa gtg aca aca tgc tcc ttc aac agc cct ctg 49
 Met Glu Glu Val Thr Thr Cys Ser Phe Asn Ser Pro Leu
 1 5 10

 20 ttc cgg cag gaa gat gac aga ggg att acc tac cgg atc cca gcc ctg 97
 Phe Arg Gln Glu Asp Asp Arg Gly Ile Thr Tyr Arg Ile Pro Ala Leu
 15 20 25

 25 ctc tac ata ccc ccc acc cac acc ttc ctg gcc ttt gca gag aag cgt 145
 Leu Tyr Ile Pro Pro Thr His Thr Phe Leu Ala Phe Ala Glu Lys Arg
 30 35 40 45

 30 tcc acg agg aga gat gag gat gct ctc cac ctg gtg ctg agg cga ggg 193
 Ser Thr Arg Arg Asp Glu Asp Ala Leu His Leu Val Leu Arg Arg Gly
 50 55 60

 35 ttg agg att ggg cag ttg gta cag tgg ggg ccc ctg aag cca ctg atg 241
 Leu Arg Ile Gly Gln Leu Val Gln Trp Gly Pro Leu Lys Pro Leu Met
 65 70 75

 40 gaa gcc aca cta ccg ggg cat cgg acc atg aac ccc tgt cct gta tgg 289
 Glu Ala Thr Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro Val Trp
 80 85 90

 45 gag cag aag agt ggt tgt gtg ttc ctg ttc ttc atc tgt gtg cgg ggc 337
 Glu Gln Lys Ser Gly Cys Val Phe Leu Phe Phe Ile Cys Val Arg Gly
 95 100 105

 50 cat gtc aca gag cgt caa cag att gtg tca ggc agg aat gct gcc cgc 385
 His Val Thr Glu Arg Gln Gln Ile Val Ser Gly Arg Asn Ala Ala Arg
 110 115 120 125

55

5	ctt tgc ttc atc tac agt cag gat gct gga tgt tca tgg agt gag gtg	433
	Leu Cys Phe Ile Tyr Ser Gln Asp Ala Gly Cys Ser Trp Ser Glu Val	
	130 135 140	
10	agg gac ttg act gag gag gtc att ggc tca gag ctg aag cac tgg gcc	481
	Arg Asp Leu Thr Glu Glu Val Ile Gly Ser Glu Leu Lys His Trp Ala	
	145 150 155	
15	aca ttt gct gtg ggc cca ggt cat ggc atc cag ctg cag tca ggg aga	529
	Thr Phe Ala Val Gly Pro Gly His Gly Ile Gln Leu Gln Ser Gly Arg	
	160 165 170	
20	ctg gtc atc cct gcg tat acc tac tac atc cct tcc tgg ttc ttt tgc	577
	Leu Val Ile Pro Ala Tyr Thr Tyr Tyr Ile Pro Ser Trp Phe Phe Cys	
	175 180 185	
25	ttc cag cta cca tgt aaa acc agg cct cat tct ctg atg atc tac agt	625
	Phe Gln Leu Pro Cys Lys Thr Arg Pro His Ser Leu Met Ile Tyr Ser	
	190 195 200 205	
30	gat gac cta ggg gtc aca tgg cac cat ggt aga ctc att agg ccc atg	673
	Asp Asp Leu Gly Val Thr Trp His His Gly Arg Leu Ile Arg Pro Met	
	210 215 220	
35	gtt aca gta gaa tgt gaa gtg gca gag gtg act ggg agg gct ggc cac	721
	Val Thr Val Glu Cys Glu Val Ala Glu Val Thr Gly Arg Ala Gly His	
	225 230 235	
40	cct gtg cta tat tgc agt gcc cgg aca cca aac agg tgc cgg gca gag	769
	Pro Val Leu Tyr Cys Ser Ala Arg Thr Pro Asn Arg Cys Arg Ala Glu	
	240 245 250	
45	gcg ctc agc act gac cat ggt gaa ggc ttt cag aga ctg gcc ctg agt	817
	Ala Leu Ser Thr Asp His Gly Glu Gly Phe Gln Arg Leu Ala Leu Ser	
	255 260 265	
50	cga cag ctc tgt gag ccc cca cat ggt tgc caa ggg agt gtg gta agt	865
	Arg Gln Leu Cys Glu Pro Pro His Gly Cys Gln Gly Ser Val Val Ser	
	270 275 280 285	

55

ttc cgg ccc ctg gag atc cca cat agg tgc cag gac tct agc agc aaa 913
 Phe Arg Pro Leu Glu Ile Pro His Arg Cys Gln Asp Ser Ser Ser Lys
 5 290 295 300

gat gca ccc acc att cag cag agc tct cca ggc agt tca ctg agg ctg 961
 Asp Ala Pro Thr Ile Gln Gln Ser Ser Pro Gly Ser Ser Leu Arg Leu
 10 305 310 315

gag gag gaa gct gga aca ccg tca gaa tca tgg ctc ttg tac tca cac 1009
 Glu Glu Glu Ala Gly Thr Pro Ser Glu Ser Trp Leu Leu Tyr Ser His
 15 320 325 330

cca acc agt agg aaa cag agg gtt gac cta ggt atc tat ctc aac cag 1057
 Pro Thr Ser Arg Lys Gln Arg Val Asp Leu Gly Ile Tyr Leu Asn Gln
 20 335 340 345

acc ccc ttg gag gct gcc tgc tgg tcc cgc ccc tgg atc ttg cac tgt 1105
 Thr Pro Leu Glu Ala Ala Cys Trp Ser Arg Pro Trp Ile Leu His Cys
 25 350 355 360 365

ggg ccc tgt ggc tac tct gat ctg gct gct ctg gag gag gag ggc ttg 1153
 Gly Pro Cys Gly Tyr Ser Asp Leu Ala Ala Leu Glu Glu Glu Gly Leu
 30 370 375 380

ttt ggg tgt ttg ttt gaa tgt ggg acc aag caa gag tgt gag cag att 1201
 Phe Gly Cys Leu Phe Glu Cys Gly Thr Lys Gln Glu Cys Glu Gln Ile
 35 385 390 395

gcc ttc cgc ctg ttt aca cac cgg gag atc ctg agt cac ctg cag ggg 1249
 Ala Phe Arg Leu Phe Thr His Arg Glu Ile Leu Ser His Leu Gln Gly
 40 400 405 410

gac tgc acc agc cct ggt agg aac cca agc caa ttc aaa agc aat 1294
 Asp Cys Thr Ser Pro Gly Arg Asn Pro Ser Gln Phe Lys Ser Asn
 45 415 420 425

taattggctt aggacccaat ttccatagat gcaaattggca gttacagaca ggtaacaga 1354

agctactgaa gtctacagat aatcaaaaaa cttaatatc tgttcctac cttttttcac 1414

ttttcctcct ccaaagagca aaatgaaaat ttgccttag ctactgcagt ggaaagagca 1474

55

ctgaactagg agttggaaga caaggatgtg gtcctggctc tgcactggct tgcttttga 1534
 5 ccttggatgt gtcacctgaa ctctctggac ctcaggtttc catctgtaaa atgagagtat 1594
 tggttctaag atttctcacc ttctcatccc taggacaagc atagtgcctg catgcttcat 1654
 10 gatcagtaag tcttggctgc ataaaggact ctgatgtcaa aatggaaacc aggggactta 1714
 ccttttcaca tgacttaccc ctcatccgag tgtgaggta caagcagtg tcatggcagg 1774
 15 aaggaagacc agatctgtat gatttgttcc atttttaata acaaaaatat ccacaccctt 1834
 ttaataatgc tcagagttct gtaggtcttc taccctagag gaattgagca aaacagcc 1892

20

<210> 4
 <211> 428
 <212> PRT
 25 <213> Homo sapiens

25

<400> 4
 Met Glu Glu Val Thr Thr Cys Ser Phe Asn Ser Pro Leu Phe Arg Gln
 30 1 5 10 15

30

Glu Asp Asp Arg Gly Ile Thr Tyr Arg Ile Pro Ala Leu Leu Tyr Ile
 35 20 25 30

35

Pro Pro Thr His Thr Phe Leu Ala Phe Ala Glu Lys Arg Ser Thr Arg
 40 35 40 45

40

Arg Asp Glu Asp Ala Leu His Leu Val Leu Arg Arg Gly Leu Arg Ile
 50 55 60

45

Gly Gln Leu Val Gln Trp Gly Pro Leu Lys Pro Leu Met Glu Ala Thr
 65 70 75 80

50

Leu Pro Gly His Arg Thr Met Asn Pro Cys Pro Val Trp Glu Gln Lys
 85 90 95

55

Ser Gly Cys Val Phe Leu Phe Phe Ile Cys Val Arg Gly His Val Thr

	100	105	110
5	Glu Arg Gln Gln Ile Val Ser Gly Arg Asn Ala Ala Arg Leu Cys Phe		
	115	120	125
10	Ile Tyr Ser Gln Asp Ala Gly Cys Ser Trp Ser Glu Val Arg Asp Leu		
	130	135	140
15	Thr Glu Glu Val Ile Gly Ser Glu Leu Lys His Trp Ala Thr Phe Ala		
	145	150	155
	Val Gly Pro Gly His Gly Ile Gln Leu Gln Ser Gly Arg Leu Val Ile		
	165	170	175
20	Pro Ala Tyr Thr Tyr Tyr Ile Pro Ser Trp Phe Phe Cys Phe Gln Leu		
	180	185	190
25	Pro Cys Lys Thr Arg Pro His Ser Leu Met Ile Tyr Ser Asp Asp Leu		
	195	200	205
30	Gly Val Thr Trp His His Gly Arg Leu Ile Arg Pro Met Val Thr Val		
	210	215	220
	Glu Cys Glu Val Ala Glu Val Thr Gly Arg Ala Gly His Pro Val Leu		
	225	230	235
35	Tyr Cys Ser Ala Arg Thr Pro Asn Arg Cys Arg Ala Glu Ala Leu Ser		
	245	250	255
40	Thr Asp His Gly Glu Gly Phe Gln Arg Leu Ala Leu Ser Arg Gln Leu		
	260	265	270
45	Cys Glu Pro Pro His Gly Cys Gln Gly Ser Val Val Ser Phe Arg Pro		
	275	280	285
	Leu Glu Ile Pro His Arg Cys Gln Asp Ser Ser Ser Lys Asp Ala Pro		
	290	295	300
50	Thr Ile Gln Gln Ser Ser Pro Gly Ser Ser Leu Arg Leu Glu Glu Glu		
	305	310	315
55			320

5 Ala Gly Thr Pro Ser Glu Ser Trp Leu Leu Tyr Ser His Pro Thr Ser
 325 330 335

Arg Lys Gln Arg Val Asp Leu Gly Ile Tyr Leu Asn Gln Thr Pro Leu
 340 345 350

10 Glu Ala Ala Cys Trp Ser Arg Pro Trp Ile Leu His Cys Gly Pro Cys
 355 360 365

15 Gly Tyr Ser Asp Leu Ala Ala Leu Glu Glu Glu Gly Leu Phe Gly Cys
 370 375 380

20 Leu Phe Glu Cys Gly Thr Lys Gln Glu Cys Glu Gln Ile Ala Phe Arg
 385 390 395 400

Leu Phe Thr His Arg Glu Ile Leu Ser His Leu Gln Gly Asp Cys Thr
 405 410 415

25 Ser Pro Gly Arg Asn Pro Ser Gln Phe Lys Ser Asn
 420 425

30 <210> 5
 <211> 10
 <212> PRT
 <213> Bos primigenius taurus

35 <220>
 <221> UNSURE
 <222> (2)
 40 <223> Xaa=ala or arg

 <220>
 <221> UNSURE
 45 <222> (3)
 <223> Xaa=glu or gly

 <220>
 50 <221> UNSURE
 <222> (4)
 <223> Xaa=ile or tyr

55

5 <220>
 <221> UNSURE
 <222> (5)
 <223> Xaa=leu or ser

10 <400> 5
 Asp Xaa Xaa Xaa Xaa Ser His Val Gln Gly
 1 5 10

15 <210> 6
 <211> 5
 <212> PRT
 20 <213> Bos primigenius taurus

25 <400> 6
 Asp Asp Leu Gly Ala
 1 5

30 <210> 7
 <211> 5
 <212> PRT
 <213> Bos primigenius taurus

35 <400> 7
 Glu Glu Val Thr Ser
 1 5

40 <210> 8
 <211> 5
 45 <212> PRT
 <213> Bos primigenius taurus

50 <400> 8
 Lys Tyr Glu Glu Leu
 1 5

55

5 <210> 9
<211> 9
<212> PRT
<213> Bos primigenius taurus

10 <400> 9
Lys Asp Glu Asp Ala Leu His Leu Val
1 5

15 <210> 10
<211> 26
<212> DNA
<213> Artificial Sequence

20 <220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide

25 <220>
<221> unsure
<222> (6,15,17,18,24)

30 <223> n=inosine

<400> 10
gaygcngara tyctnwnnca ygtinca 26

35 <210> 11
<211> 29
<212> DNA
<213> Artificial Sequence

40 <220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide

45 <220>
<221> unsure
<222> (6,12,13,15,24)

50 <223> n=inosine

55

5 <400> 11
 ccctgnacrt gnnwnagrat tycngertc 29

10 <210> 12
 <211> 29
 <212> DNA
 <213> Artificial Sequence

15 <220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide

20 <220>
 <221> unsure
 <222> (4,6,9,13,15,17,18,24)
 <223> n=inosine

25 <400> 12
 gayngggnt aynsnwnnca ygtncaggg 29

30 <210> 13
 <211> 29
 <212> DNA
 <213> Artificial Sequence

35 <220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide

40 <220>
 <221> unsure
 <222> (6,11,12,14,16,21,24,25)
 <223> n=inosine

45 <400> 13
 ccctgnacrt gnnwnsrta nccncrta 29

50
 55

5 <210> 14
<211> 14
<212> DNA
<213> Artificial Sequence

10 <220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide

15 <220>
<221> unsure
<222> (9,11)
<223> n=inosine

20 <400> 14
gaygayctng gngc 14

25 <210> 15
<211> 14
<212> DNA
30 <213> Artificial Sequence

35 <220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide

40 <220>
<221> unsure
<222> (3,6)
<223> n=inosine

45 <400> 15
gcncnagrt crtc 14

50 <210> 16
<211> 15
<212> DNA
55 <213> Artificial Sequence

5 <220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide

<220>
<221> unsure
10 <222> (1,3,4,7)
<223> n=inosine

<400> 16
15 nsnnngtnacy tcytc 15

<210> 17
20 <211> 15
<212> DNA
<213> Artificial Sequence

25 <220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide

30 <220>
<221> unsure
<222> (1,3)
<223> n=inosine

35 <400> 17
nanytcytcr taytt 15

40 <210> 18
<211> 26
<212> DNA
45 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide
50 <220>

5 <221> unsure
 <222> (15,18,24)
 <223> n=inosine

 <400> 18
 aargaygarg aygcncnca yctngt 26
 10

 <210> 19
 <211> 23
 15 <212> DNA
 <213> Artificial Sequence

 <220>
 20 <223> Description of Artificial Sequence:synthetic
 oligonucleotide

 <220>
 25 <221> unsure
 <222> (3,9,11)
 <223> n=inosine

 30 <400> 19
 acnagrtgna gngcrtcytc rtc 23

 35 <210> 20
 <211> 8
 <212> PRT
 <213> Unknown
 40
 <220>
 <223> Description of Unknown Organism:consensus sequence

 45 <220>
 <221> UNSURE
 <222> (2,4,6)
 <223> Xaa=optional amino acid
 50
 <400> 20
 Ser Xaa Asp Xaa Gly Xaa Thr Trp
 55

1 5

5

<210> 21
<211> 30
<212> DNA
<213> Artificial Sequence

10

<220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide

15

<400> 21
cccgaattcg tcattggaaga agtgacatca

20

30

<210> 22
<211> 30
<212> DNA
<213> Artificial Sequence

25

<220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide

30

<400> 22
cccgaattct tactttttac ttggctcaga

35

30

<210> 23
<211> 27
<212> DNA
<213> Artificial Sequence

40

<220>
<223> Description of Artificial Sequence:synthetic
oligonucleotide

45

<400> 23
ggacaccgga ccattgaaccc ctgtcct

50

27

55

<210> 24
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:synthetic
 oligonucleotide

<400> 24
 cctggcccca cagcaaaagt ggccca

26

Claims

1. A protein defined in the following (A) or (B):

(A) a protein which has the amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4, or
 (B) a protein which has the amino acid sequence including substitution, deletion, insertion, or transition of one
 or several amino acid residues in SEQ ID NO: 2 or SEQ ID NO: 4, and exhibits activity to eliminate a sialic acid
 residue from a non-reducing terminal of ganglioside.

2. A DNA coding for a protein defined in the following (A) or (B):

(A) a protein which has the amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4, or
 (B) a protein which has the amino acid sequence including substitution, deletion, insertion, or transition of one
 or several amino acid residues in SEQ ID NO: 2 or SEQ ID NO: 4, and exhibits activity to eliminate a sialic acid
 residue from a non-reducing terminal of ganglioside.

3. The DNA according to claim 2 which has the nucleotide sequence of SEQ ID NO: 1 or SEQ ID NO: 3.

Peptide	Amino acid sequence	Sense primer	Antisense primer
DN1-1	DAEILSHVQg RGYS (SEQ ID NO 5)	GAYGCGARATYCTIWIICAYGTICA (SEQ ID NO 10) GAYTGIGGIT AYISIWICA YGTICAGGG (SEQ ID NO 12)	CCCTGIACRT GIWIAGRAT TYCIGCRIC (SEQ ID NO 11) CCCTGIACRT GIWISIRTA ICCICIRIC (SEQ ID NO 13)
DN-2	DdIga (SEQ ID NO 6)	GAYGAYCTIG GIGC (SEQ ID NO 14)	GCICCIAGRT CRIC (SEQ ID NO 15)
DN-3	EEVtS (SEQ ID NO 7)		ISIIGTIACY TCYTC (SEQ ID NO 16)
AP-1	(K)yeeI (SEQ ID NO 8)		IAIYTCYTCR TAYTT (SEQ ID NO 17)
AP-3	(K)DEDAIhIv (SEQ ID NO 9)	AARGAYGARG AYGCICTICA YCTIGT (SEQ ID NO 18)	ACIAGRTGIA GIGCRTCYTC RTC (SEQ ID NO 19)

Fig. 1

49' KDEDALHLVLRRG--L 88mSD
 . * .***

1' METCPVLQKETLFHTEVYAYRIPALLYLKKQKTLLAFAEKRASRTDEHAELIVLRRGSYN RMcSD

63' RTGQSVQWEPLKSLMKATLPGHRTMNPVWERKSGYVYLFFICVQGHVTERQQIMSGRN 88mSD
 ... *. * . * * ***.*****..... .**** *. *. *. *.. *

61' GATNHVKWQPEEVVTOAQLEGHRSMNPCLYDKQTKTLFLFFI AVPGRVSEQHQLQTRVN RMcSD

123' AARLCFICSDAGHSWSDVRDLTEEVIQPEVTHWATFAVQPGHG1QL--QSGRLIIPAYA 88mSD
 ..***. * * * .** *.****..**.. .*****. ** ..*. *..***

121' VTRLCRVTSTDYGMNWSPVQDLTETTIGSTHQDWATFAVQPGHCLQLRN RAGSLLVPAYA RMcSD

181' YYIPFWFFCFRLPYRARPHSLMIYSDDL 88mSD
 *

181' YRKLHPVHKPTPFAFCFISLDHGHTWELGNFVSENSLECQVAEVGTGAHRVVYLNARSI RMcSD

Fig. 2

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP98/02072

A. CLASSIFICATION OF SUBJECT MATTER Int.Cl ⁶ C12N9/24, C12N15/56, C12N5/10 // (C12N9/24, C12R1:91)		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols) Int.Cl ⁶ C12N9/24, C12N15/56, C12N5/10		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) WPI (DIALOG), BIOSIS (DIALOG), EMBL, Genbank, DDBJ, GeneSeq		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
PX	J. Biochem. 123 [5] (01. 05. 98) K. Hata et al., "Purification and Characterization of a Membrane-Associated Ganglioside Sialidase from Bovine Brain" p.899-905	1-3
PX	Eur. J. Biochem. 248 [2] (09. 97) J. Kopitz et al., "Partial characterization and enrichment of a membrane-bound sialidase specific for gangliosides from human brain tissue" p.527-534	1-3
A	J. Biochem. 107 (1990) T. Miyagi et al., "Biochemical and Immunological Studies on Two Distinct Ganglioside-hydrolyzing Sialidase from apticulate Fraction of Rat Brain" p.787-793	1-3
<input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
<p>* Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, each combination being obvious to a person skilled in the art</p> <p>"Z" document member of the same patent family</p>		
Date of the actual completion of the international search July 31, 1998 (31. 07. 98)		Date of mailing of the international search report August 11, 1998 (11. 08. 98)
Name and mailing address of the ISA/ Japanese Patent Office		Authorized officer
Facsimile No.		Telephone No.

Form PCT/ISA/210 (second sheet) (July 1992)